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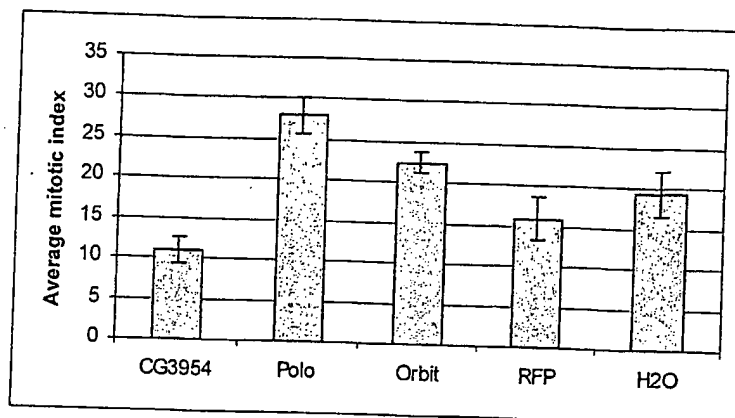
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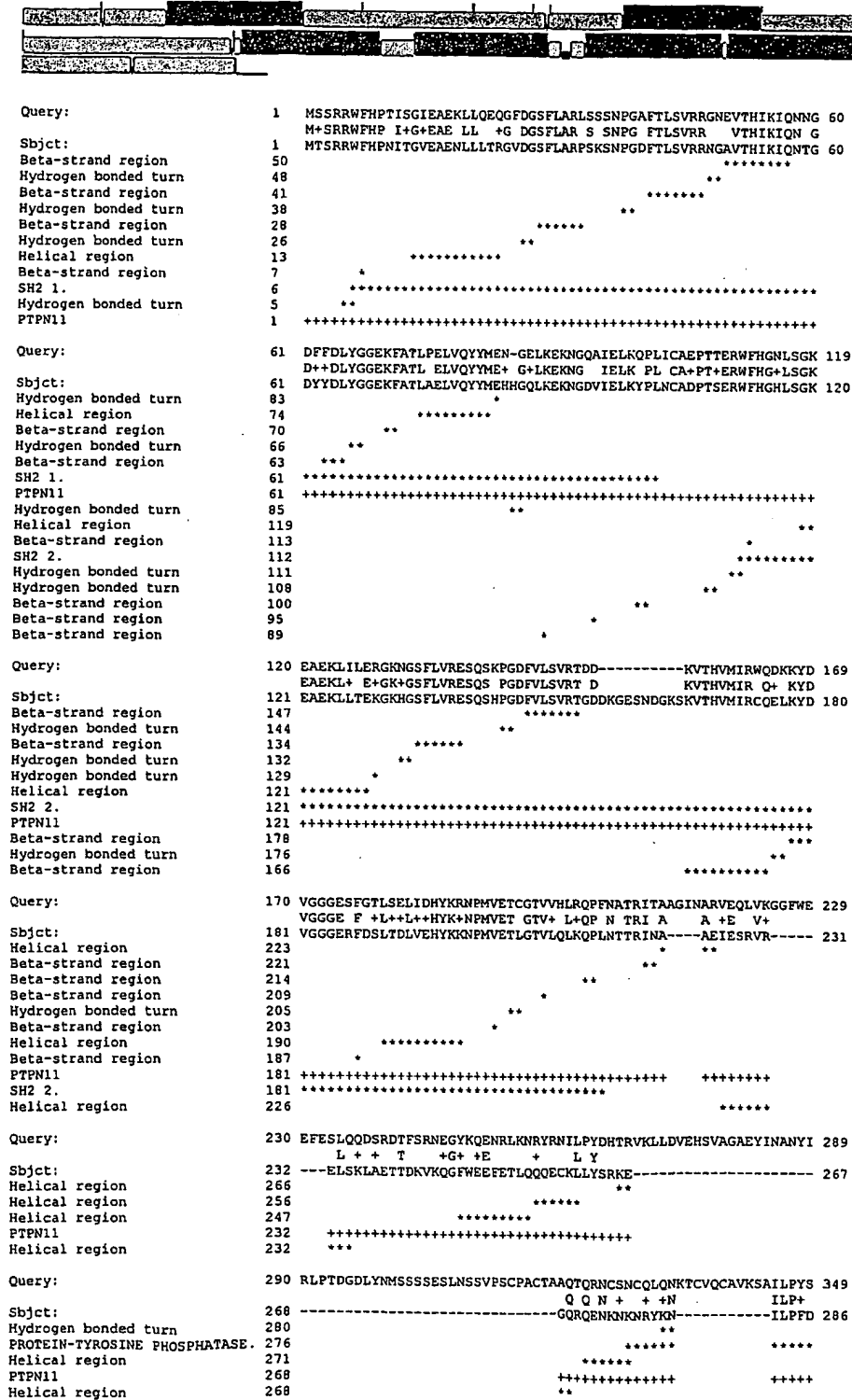
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**FIGURE 1**

## FIGURE 2

Score = 553 bits (1425), Expect = e-156  
 Identities = 327/700 (46%), Positives = 406/700 (57%), Gaps = 152/700 (21%)



```

Hydrogen bonded turn      286

Query:                    350 NCATCSRKSDSLSKHKRESSASSPSSGSGSPGSSSGTSGVSSVNGPPTNLTSGTAG 409
      +      D      P P +
Sbjct:                    287 HTRVVLHDGD-----PNEPVS----- 302
Beta-strand region       289 ***
Hydrogen bonded turn     287 **
PTPN11                   287 ++++++++
PROTEIN-TYROSINE PHOSPHATASE. 287 *****

Query:                    410 CLVGLLKRHSNDSSGAVSISMAERERE-REREMFKTYIATQGCLLTQQVNTVDFWNRMVN 468
      D A + I M E E + + K+YIATQGCL NTV DFW MV+
Sbjct:                    303 -----DYINA-NIIMPEFETKCHNSKPKKSYIATQGCLQ-----NTVNDFWRMVF 346
Beta-strand region       304 ****
PTPN11                   303 ++++++
PROTEIN-TYROSINE PHOSPHATASE. 303 *****
Hydrogen bonded turn     335
Beta-strand region       327 ****
Helical region           338

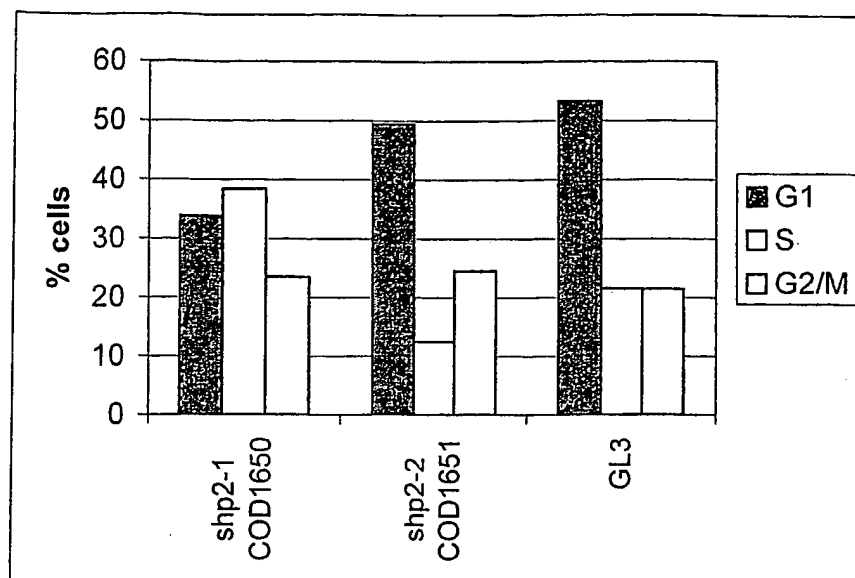
Query:                    469 QENTRVIIVMTTKEYERGKCKARYWPDGRSEQFGHARIQCVSENSTSDYTLREFLVSWR 528
      QEN+RVIVMTTKE ERGK KC +YWPDE ++G R++ V E++ DYTLE +S
Sbjct:                    347 QENSRVIVMTTKEVERGKSKVKYWPDEYALKEYGVMRVRNVKESAAHDYTLRELKLSKV 406
Hydrogen bonded turn     406
Beta-strand region       396
Beta-strand region       383
Hydrogen bonded turn     381
Beta-strand region       377
Hydrogen bonded turn     374
Beta-strand region       364
Hydrogen bonded turn     362
Beta-strand region       360
Beta-strand region       352
Hydrogen bonded turn     349
Helical region           347 **
PTPN11                   347 ++++++
PROTEIN-TYROSINE PHOSPHATASE. 347 *****

Query:                    529 DQ--PARRIFHYHFQVWPDHGVDPGCVLNFQLQDVNTRQSHLAQAGEKPGPICVHCSAG 586
      Q R ++ YHF+ WPDHGV+DPG VL+FL+V+ +Q + AG P+ VHCSAG
Sbjct:                    407 GQGNTERTVWQYHFTWPDHGVPSDPGGVLDGLEEVHKKQESIMDAG----PVVHCSAG 462
Beta-strand region       408
Hydrogen bonded turn     407 *
PTPN11                   407 ++++++
PROTEIN-TYROSINE PHOSPHATASE. 407 *****
Hydrogen bonded turn     450
Helical region           432
active                   459
Beta-strand region       455

Query:                    587 IGRGTGFIVIDMILDQIVRNLDTIDEIORTIQMVRSQRSGLVOTEAQYKFVYVAVQHYI 646
      IGRGTGFIVID++++D I G+D +ID+ +TIQMVRSQRSGLVOTEAQY+FY AVQHYI
Sbjct:                    463 IGRGTGFIVIDILIDIIREKGVDCDIDVPKTIQMVRSQRSGLVOTEAQYREIYMAVQHYI 522
Helical region           508
Hydrogen bonded turn     502
Hydrogen bonded turn     499
Helical region           490
Beta-strand region       487
Hydrogen bonded turn     484
Helical region           464
PTPN11                   463 ++++++
PROTEIN-TYROSINE PHOSPHATASE. 463 *****

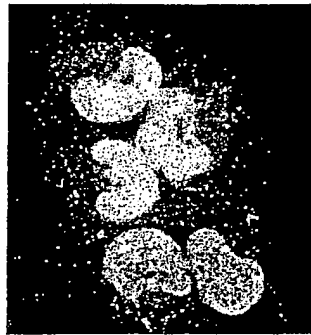
Query:                    647 QTLIARKRAEQSLQVGREYTNIKYTGEIGNDSQRSPLPP 686
      +TL R E++S + G EYTNIKY+ +SPLPP
Sbjct:                    523 ETLQRRIEEBKSKRGHEYTNIKYSLADQTSQDQSLPP 562
Conflict                  548
phosphorylation          542
Conflict                  535
Hydrogen bonded turn     524 *
Helical region           523 *
PTPN11                   523 ++++++

```

**FIGURE 3**

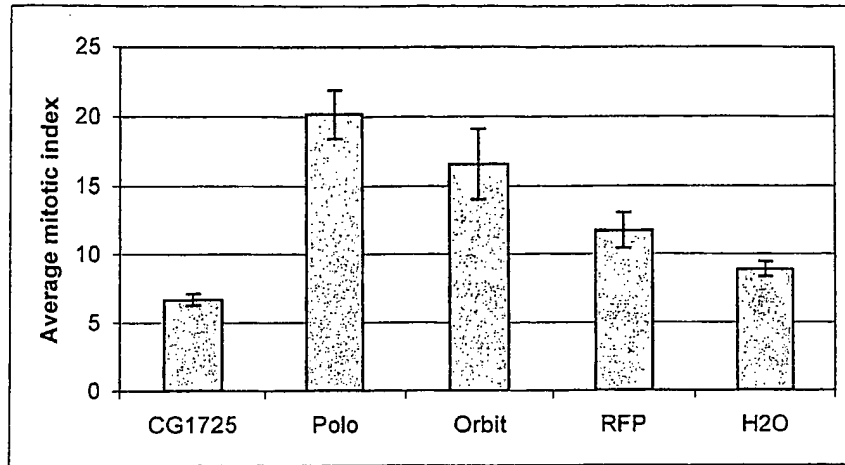
**FIGURE 4**

A)



B)




**FIGURE 5**

# FIGURE 6A

Sequence alignment of Dros Dlg1 and Hu Dlg homolog 1

## BLAST P sequence alignment

Score = 616 bits (1588), Expect = e-175  
Identities = 306/517 (59%), Positives = 390/517 (75%), Gaps = 24/517 (4%)



```

Query: 453 QPGSRYASTNVLAAVPPGTPRAVST-----EDITREPTITITQKGPQGLGFNIVGGE 504
          QP  + S +      P +P  S          ++ITREPR + + +G GLGFNIVGGE
Sbjct: 425 QPVDNHVSPSSFLGQTPASPARYSPVSKAVLGDDEITREPRKVVLRHGSTGLGFNIVGGE 484

Query: 505 DGQGIYVSFILAGGPADLGSSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGGVVTLAQ 564
          DG+GI++SFILAGGPADL EL++GD+++SVN+V+L A+HE+AA ALK +G VT++AQ
Sbjct: 485 DGEGIFISFILAGGPADLGSSELKRGDRIISVNSVDLRAASHEQAAAALKNAGQAVTIVAQ 544

Query: 565 YRPEEYNRFEARIQELKQXXXXXXXXXXXX-XXQKRSLYVRALFDYDPNRDDGLPSRG 623
          YRPEEY+RFEA+I +L++Q          QKRSLYVRALFDYD +D GLPS+G
Sbjct: 545 YRPEEYSRFEAKIHDLREQMNNSSISSGSGSLRTSQKRSLYVRALFDYDKTKDSGLPSQG 604

Query: 624 LPFKHGDILHVTNASDDEWQARRVLGDNEDQIGIVPSKRRWERKMRARDRSVKFQGH 683
          L FK GDILHV NASDDEWQAR+V D E +++G++PSKRR E+K RAR ++VKF
Sbjct: 605 LNFKFGDILHVINASDDEWQARQVTPDGESDEVGVIPSKRRVEKKERARLKTVKFN--- 661

Query: 684 AANNLNDKQSTLDRKKKNFTFSRKFFPMKSRDEKNEDGSDQEPNGVVSSTSEIDIXXXX 743
          + DK + + K+K FSRKFPF K++D+ ++ SD + + V S+ S+ +
Sbjct: 662 --SKTRDKGQSFNDKRRKNLFSRKFPF FYKNKDQSEQETSDADQH-VTSNASDSE----- 712


Query: 744 XXXXXXXXXXXXXVLSYEAVQRLSINYTRPVIIILGPLKDRINDDLISEYDPKFGSCVPHTT 803
          VLSYE V + +NYTRPVIIILGP+KDRINDDLISE+PDKFGSCVPHTT
Sbjct: 713 ---SSYRQEEYVLSYEPVNQEEVNYTRPVIIILGPMKDRINDDLISEFPDKFGSCVPHTT 769

Query: 804 RPKREYVDGRDYHFVSSREQMERDIQNLHFIAGQYNDNLYGTSVASVREVAEKGKHCI 863
          RPKR+YEVGDRDYHFV+SREQME+DIQ H FIEAGQYN++LYGTSV SVREVA KGKHCI
Sbjct: 770 RPKRDYVDGRDYHFVTSREQMEKDIQEHKFIAGQYNNHLYGTSVQSVREVAGKGKHCI 829

Query: 864 LDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNRRMTEEQAQKTYERAQKMEQEFGEY 923
          LDVSGNAIKRLQ+AQLYP+++FIKPKS+++MEMN+R+TEEQA+KT+ERA+K+EQEF E+
Sbjct: 830 LDVSGNAIKRLQIAQLYPISIFIKPKSMENIMEMNKRLEEQARKTFERAMKLEQEFTEH 889

Query: 924 FTGVVQGDITIEEYISKVKSMIWSQSGPTIWPVPSKESL 960
          FT +VQGD+T+E+IY++VK +I QSG IWVP+KE L
Sbjct: 890 FTAIVQGDITLEDIYNQVKQIIEEQSGSYIWPVPAKEKL 926
Score = 206 bits (524), Expect = 2e-51
Identities = 119/227 (52%), Positives = 146/227 (63%), Gaps = 30/227 (13%)

```



```

Query: 24 LFNLD-----VNGDDS-WLYEDIQLERGNGLGFSIAGGTDNPHIGTDTSIYITKLIS 76
          L N DS      VNG D+ + YE+I LERGNGLGFSIAGGTDNPHIG D+SI+ITK+I+
Sbjct: 201 LVNTDSLETPTYVNGTDADYEYEEITLERGNGLGFSIAGGTDNPHIGDSSIFITKIIT 260

Query: 77 GGAAAADGRLXXXXXXXXXXXXXXXXXPHASAVDALKKAGNVVVKLHVKKRXXXXXXXXXXXX 136
          GGAAA DGR L      H+ AV+ALK+AG++V+L+VKK+
Sbjct: 261 GGAAADGRLRVNDCILQVNEVDVRDVTHSKAVEALKEAGSIVRLYVKKRKPVS----- 315

Query: 137 XXXXXXXXXXXXXKVIEIDLKGGKGLGFSIAGGIGNQHIPGDNGIYVTKLTDGGRAQV 196
          K++EI L+KG KGLGFSIAGG+GNQHIPGDN IYVTK+ +GG A
Sbjct: 316 -----KIMEIKLIKPKGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAHK 361

```



Query: 197 DGRLSIGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLIIGK 243  
 DG+L IGDKL+AV + LE VTHE AV LK+ +D V L + K  
 Sbjct: 362 DGKLGIGDKLLAV---NNVCLEEVTHEEAVTALKNTSDFVYLKVAK 404  
 Score = 88.2 bits (217), Expect = 7e-16  
 Identities = 68/234 (29%), Positives = 95/234 (40%), Gaps = 43/234 (18%)

Query: 40 DIQLERGNGLGFSIAGGTDNPHIGTDTSIYITKLISGGAAAADGRLXXXXXXXXXXXXX 99  
 +I+L +G GLGFSIAGG N HI D SIY+TK+I GGAA DG+L  
 Sbjct: 319 EIKLIKGPGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAHKDGKLGIGDKLLAVNNVC 378

Query: 100 XXXXPHASAVDALCKAGNVVVLHVKKRXXXXXXXXXXXXXXXXXXXXXKVI----- 153  
 H AV ALK + V L V + V  
 Sbjct: 379 LEEVTHEEAVTALKNTSDFVYLKVAKPTSMYNDGYAPPDITNSSSQPVNDHVSPPSFLG 438

Query: 154 -----EIDLKGGKGLGFSIAGGIGNQHIPGDNGIYVT 186  
 ++ L +G GLGF+I GG + GI+++  
 Sbjct: 439 QTFASPARYSPVSKAVLGDDEITREPRKVVLRHGSTGLGFNIVGGEDGE-----GIFIS 492

Query: 187 KLTGGRAGVDGRLSIGDKLIAVRTNGSEKNLENVTHELAVATLKSITDKVTLI 240  
 + GG A + G L GD++I+V + +L +HE A A LK+ VT++  
 Sbjct: 493 FILAGGPADLSGELRKGDRISV---NSVDLRAASHEQAAAALKNAGQAVTIV 542  
 Score = 70.1 bits (170), Expect = 2e-10  
 Identities = 47/141 (33%), Positives = 69/141 (48%), Gaps = 12/141 (8%)

Query: 432 MPALPVESNQTNNRSQSPQPRQPGSRYASTNVLAAPPGTTPRAVSTEDITREPTITIQQ 491  
 +P LPV + T PQ P +T+ L TP V+ D E IT+++  
 Sbjct: 176 IPVLPVPAENTVILFTIPQANPPPVLVNTDSLE-----TPTYVNGTDADYEYEEITLER 229

Query: 492 GPQGLGFNIVGGEDG-----QGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATH 545  
 G GLGF+I GG D I+++ I+ GG A L+ D +L VN V++ TH  
 Sbjct: 230 GNSGLGFSIAGGTDNPHIGDDSSIFITKIITGGAAQDGRLRVNDCLQVNEVDVRDVTH 289

Query: 546 EEAAQALKTSGGVVTLQAQR 566  
 +A +ALK +G +V L + R  
 Sbjct: 290 SKAVEALKEAGSIVRLYVKRR 310  
 Score = 67.4 bits (163), Expect = 1e-09  
 Identities = 39/81 (48%), Positives = 49/81 (60%), Gaps = 6/81 (7%)

Query: 487 ITIQKGPQGLGFNIVGGEDGQ-----GIYVSFILAGGPADLGSELKRGDQLLSVNNVNL 540  
 I + KGP+GLGF+I GG Q IYV+ I+ GG A +L+ GD+LL+VNNV L  
 Sbjct: 320 IKLIKGPGLGFSIAGGVGNQHIPGDNSIYVTKIIEGGAHKDGKLGIGDKLLAVNNVCL 379

Query: 541 THATHEEAQALKTSGGVVTL 561  
 THEEA ALK + V L  
 Sbjct: 380 EEVTHEEAVTALKNTSDFVYL 400

## FIGURE 6B

## CLUSTAL W (1.82) sequence alignment

```

Drosophila  MTTRKKKRDGGSGGGGFIKKVSSLFNLDVNGDDSWLYEDIQLERGNSSGLGFSIAGGTDN 60
Human       MPVRKQD-----TQRALHLLLEYRSKLSQTEDRQLRSSIERVINIFQSNLFQ 47
*..*:.      .. :.*.  ..  ** *.  . . :  : . . :

Drosophila  PHIGTDTSIYITKLISGGAAAADGRLSINDIIVSVNDVSVVDVPHASAVDALKKAGNVVK 120
Human       ALIDIQEFYEVTLTDN--PKCID-RSKPSEPIQPVNTWEISSLPSTVTSETLPSSLSPS 104
. *. :      : * * . . . * * . . : * . ** . : : * : : . . . : .

Drosophila  LHVKKRGTATTPAAGSAAGDARDSAASGPKVIEIDLKGGKGLGFSIAGGIGNQHHPGD 180
Human       VEKRYQDEDTPPQEHISP--QITNEVIGPELVHVSEKN--LSEIENVHGFVSHSHIS-P 159
: . * : . . * . * : . . : . . : . . : . . : . . : . . : . . : . . :

Drosophila  NGIYVTKLTDGGRAQVDGRLSIGDKLIAVRTNGSEKN---LENVTHELAVATLKSITDKV 237
Human       IKPTEAVLPSPPTVPVLPVPAENTVILPTIPQANPPPVLVNTDSLETPTYVNGTDAD 219
: * . . . * . * : . : . : . : . * : . * . * . * . * . * . * . * .

Drosophila  TLIIGKTQHLTTSAS----GGGGGLSSGQQLSQSQSLATSQSQSQVHQHQQHATPMVNS 293
Human       YEYEEITLERGNSSGLGFSIAGGTDNPHIGDDSSIFITKIITGGAAQDGRLRVNDICILQV 279
* . . * . . ** . . * : * : : * . : : * : : : : : : : : : : : :

Drosophila  QSTGALNSMGQTVVDSPSIPQAAAATAANASASASVIASNNNTISNTTVTVTATATAS 353
Human       NEVDVRDVTSHKAVEALKEAGSIVRLYVKKRPVSEKIMEIK-LIKGPKGLGFSIAGGVG 338
: . . . : . . . * : . . : . . : . . * . : : * . . . : : . . .

Drosophila  NDSSKLPPSLGANSSISISNSNSNSNNINNINSINNNSSSSSSTTATVAATPTAASA 413
Human       NQHHPGDNISYVTKIIEGGAHKDGKLGKLLAVNNVCLEEVTHEEAVTALKNTSDFV 398
* :      * : . . . * . . : : : : : : : : : : : : : : * : * . * : .

Drosophila  AAAAASSPPANSFYNNASMPALVESNQTNNRSQSPQPRQPGSRYASTNVLAAPVPGTPR 473
Human       YLKVAK-PTSMYMDGYAPPDITNSSSQPVNDHVSFSS-FLGQTPASP---ARYSPVSKA 453
. * . * : : . : * : . * . * . . * . . * . * . * . * . * . * .

Drosophila  AVSTEDITREPTITIQKGPQGLGFNIVGGEDGQGIYVSFILAGGPADLGSELKRGDQLL 533
Human       VLGDDEITREPRKVVLRHGSTGLGFNIVGGEDGEGIFISFILAGGPADLSGELRKGDRII 513
. . : : * : * : . : : : * . * : * : * : * : * : * : * : * : * : * :

Drosophila  SVNNVNLTHATHEEAQALKTSGGVVTLAQRPEEYNRFEARIQELKQQAALGAGGSGT 593
Human       SVNSVDLRAASHEQAAAALKNAGQAVTIVAQRPEEYSRFEAKIHDLEQMMNSSISSGS 573
* * . * . * : * : * . * . * : * . * : * : * : * : * : * : * : * :

Drosophila  -LLRTTQKRSLYVRALFDYDPNRDGLPSRGLPFKHGDIHVHTNASDDEWQARRVLGDN 652
Human       GSLRTSQKRSLYVRALFDYDKTKDSGLPSQGLNFKFGDILHVINASDDEWQARRQVTPDG 633
* * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * :

Drosophila  EDEQIGIVPSKRRWERKMRARDRSVKFQGHAAANNLQKQSTLDRKKKNFTFSRKFPPFMK 712
Human       ESDEVGVIPSKRRVEKKERARLKTVKFN-----SKTRDKGQSFNDRKKKNLFSRKFPPFYK 688
* . : : * : * : * : * . * . * : * : . . * . * : : * : * : * : * .

Drosophila  SRDEKNEDGSDQEPNGVVSSTSEIDINNVMNNQSNQSEENVLSYEAVQRLSINYTRP 772
Human       NKDQSEQETSADQDQ-HVTSNADSESSYRQ-----EYVLSYEPVNNQEVNTRP 738
. * : : : * : : : * . * : : . : . : . . * . * : * : * : * : * :

Drosophila  VIILGPKLDRINDDLISEYDPKFGSCVPHTTRPKREYVDGRDHFVSSREQMERDIQNH 832
Human       VIILGPKMDRINDDLISEYDPKFGSCVPHTTRPKRDYEVVDGRDHFVTSREQMEKDIQEH 798
* * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * :

Drosophila  LFIEAGQYNDNLYGTSVASVREVAEKGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVD 892
Human       KFIEAGQYNNHLYGTSVQSVREVAGKGCILVSGNAIKRLQIAQLYPISIFIKPKSME 858
* * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * :

Drosophila  SVMEMNRRMTEEQAKKTYERAIMEQEFGEYFTGVVQGDITIEEYISKVKSMIWSQSGPTI 952
Human       NIMEMNKRLEEQARKTFERAMKLEQEFTEHFTAIVQGDITLEDIYNQVKQIEEQSGSYI 918
. : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * :

```

10/19

Drosophila  
Human


WVPSKESL 960  
WVPAKEKL 926  
\*\*\*:\*\*\*.\*

## FIGURE 6C

### Sequence alignment of Dros Dlg1 and Hu Dlg homolog 2

#### BLASTP sequence alignment

Score = 621 bits (1601), Expect = e-176  
Identities = 318/524 (60%), Positives = 390/524 (73%), Gaps = 43/524 (8%)



```

Query: 438 ESNQTNRSQSPQPRQPGSRYASTNVLAAPPPTPRAVSTEDITREPRTITIQKGPQGLG 497
          +S. T++ S RQP RAVS E EPR + + KG GLG
Sbjct: 389 DSEMTSHSQHSTATRQPSMTLQ-----RAVSLEG---EPRKVVLHKGSTGLG 432

Query: 498 FNIVGGEDGQGIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGG 557
          FNIVGGEDG+GI+VSFILAGGPADL EL+RGDQ+LSVN ++L A+HE+AA ALK +G
Sbjct: 433 FNIVGGEDGEGIFVSFILAGGPADLSGELQRGDQILSVNGIDLRGASHEQAAAALKGAGQ 492

Query: 558 VVTLAQYRPEEYNRFEARIQELKQXXXXXXXXXXXXXXXXX-QKRSLYVRALFDYDPNRD 616
          VT++AQY+PE+Y RFEA+I +L++Q QKRSLYVRA+FDYD ++D
Sbjct: 493 TVTIIAQYQPEDYARFEAKIHDLREQMMNHSMSGSGSLRTNQKRSLYVRAMFDYDKSKD 552

Query: 617 DGLPSRGLPFPKHGDILHVTNASDDEWWQARRVLGDNEDEQIGIVPSKRRWERKMRARDS 676
          GLPS+GL FK+GDILHV NASDDEWWQARRV+ + + E++G++PSKRR ERK RAR ++
Sbjct: 553 SGLPSQGLSFKYGDILHVINASDDEWWQARRVMLEGDSEEMGVIPSKRRVERKERARLKT 612

Query: 677 VKFQGHAAANNLDKQSTLDRKKKNFTFSRKFFPMKSRDEKNEGSDQEPNGVVSSTSEI 736
          VKF ++ K S D++KK+F FSRKFPP K++++ ++ SD E +
Sbjct: 613 VKFNAKPGVIDS--KGSFNDKRKKSFIKSRKFFPYKNKEQSEQETSDPE-----RGQE 663


Query: 737 DIXXXXXXXXXXXXXXXXXXVLSYEAVQRLSINYTRPVIILGPLKDRINDDLISEYDPKFG 796
          D+ +LSYE V R INYTRPVIILGP+KDRINDDLISE+PDKFG
Sbjct: 664 DL-----ILSYEPVTRQEINYTRPVIILGPMKDRINDDLISEFPDKFG 706

Query: 797 SCVPHTTRPKREYVDGRDYHFVSSREQMERDIQNHLFIEAGQYNDNLYGTSVASVREVA 856
          SCVPHTTRPKR+YEVDRDYHFV SREQME+DIQ H FIEAGQYNDNLYGTSV SVR VA
Sbjct: 707 SCVPHTTRPKRDYEVDRDYHFVISREQMEKDIQEHKFIEAGQYNDNLYGTSVQSVRFVA 766

Query: 857 EKGKHCILDVSGNAIKRLQVAQLYPVAVFIKPSVDSVMEMNRRMTEEQAKKTYERAIRM 916
          E+GKHCILDVSGNAIKRLQVAQLYP+A+FIKP+S++S+MEMN+R+TEEQAKKTY+RAIK+
Sbjct: 767 ERGKHCILDVSGNAIKRLQVAQLYPIAIFIKPRSLSLMEMNKRRLTEEQAKKTYDRAIKL 826

Query: 917 EQEFGEYFTGVVQGDTEIEIYSKVKSMIWSQSGPTIWVPSKESL 960
          EQEFGEYFT +VQGDTE+IY++ K +I QSGP IW+PSKE L
Sbjct: 827 EQEFGEYFTAIVQGDTELDIYNQCKLVIEEQSGPFIWIPSKEL 870
Score = 197 bits (502), Expect = 7e-49
Identities = 111/221 (50%), Positives = 140/221 (63%), Gaps = 24/221 (10%)

```



```

Query: 23 SLFNLDVNGDD-SWLYEDIQLERGNGLGFSIAGGTDNPHIGTDSIYITKLISGGAAA 81
          +L + VNG + + +E+I LERGNGLGFSIAGGTDNPHIG D I+ITK+I GGAAA
Sbjct: 80 TLDTIPYVNGTEIEYEFEEITLERGNGLGFSIAGGTDNPHIGDDPGIFITKLIIPGGAAA 139

Query: 82 ADGRLXXXXXXXXXXXXXXXXXPHASAVDALKKAGNVVKLHVKRXKXXXXXXXXXXXXXXXXX 141
          DGRL H+ AV+ALK+AG++ +L+V+R+
Sbjct: 140 EDGRLRVNDCILRVNEVDVSEVSHSKAVEALKEAGSIARLYVRRRRPILET----- 190

Query: 142 XXXXXXXXXXXXVIEIDLVGKGGKGLGFSIAGGIGNQHIPGDNGIYVTKLTDGGRAQVDGRLS 201

```

V+EI L KG KGLGFSIAGG+GNQHIPGDN IYVTK+ DGG AQ DGRL  
 Sbjct: 191 -----VVEIKLFGKPKGLGFSIAGGVGNQHIPGDNSIYVTKIIDGGAAQKDGRLQ 240

Query: 202 IGDKLIIVRTNGSEKNLENTHELAVATLKSIDKVTLIIG 242  
 +GD+L+ V + +LE VTHE AVA LK+ ++ V L +G  
 Sbjct: 241 VGDRLLMV----NNYSLEEVTHEEAVAILKNTSEVVYLKVG 277  
 Score = 66.2 bits (160), Expect = 3e-09  
 Identities = 40/125 (32%), Positives = 64/125 (51%), Gaps = 11/125 (8%)

Query: 448 SPQPRQPGSRYASTNVLAAPPGTPRAVSTEDITREPTITIQKGPQGLGFNIVGGEDGQ 507  
 SP P +T+ L +P V+ +I E IT+++G GLGF+I GG D  
 Sbjct: 65 SPLKASPAPIIVNTDTLDTIP-----YVNGTEIEYEFEEITLERGNSGLGFSIAGGTDNP 119

Query: 508 -----GIYVSFILAGGPADLGSELKRGDQLLSVNNVNLTHATHEEAAQALKTSGGVVTL 561  
 GI+++ I+ GG A L+ D +L VN V+++ +H +A +ALK +G + L  
 Sbjct: 120 HIGDDPGIFITKIIPGGAAAEDGRLRVNDCILRVNEVDVSEVSHSKAVEALKEAGSIARL 179

Query: 562 LAQYR 566  
 + R  
 Sbjct: 180 YVRRR 184  
 Score = 65.5 bits (158), Expect = 5e-09  
 Identities = 38/81 (46%), Positives = 47/81 (57%), Gaps = 6/81 (7%)

Query: 487 ITIQKGPQGLGFNIVGGEDGQ-----GIYVSFILAGGPADLGSELKRGDQLLSVNNVNL 540  
 I + KGP+GLGF+I GG Q IYV+ I+ GG A L+ GD+LL VNN +L  
 Sbjct: 194 IKLFGKPKGLGFSIAGGVGNQHIPGDNSIYVTKIIDGGAAQKDGRLQVGDRLLMVNNYSL 253

Query: 541 THATHEEAAQALKTSGGVVTL 561  
 THEEA LK + VV L  
 Sbjct: 254 EEVTHEEAVAILKNTSEVVYL 274  
 Score = 50.8 bits (120), Expect = 1e-04  
 Identities = 33/87 (37%), Positives = 48/87 (54%), Gaps = 10/87 (11%)

Query: 154 EIDLKGGKGLGFSIAGGIGNQHIPGDNGIYVTKLTDGGRAQVDGRLSIGDKLIIVRTNG 213  
 ++ L KG GLGF+I GG + GI+V+ + GG A + G L GD+++V NG  
 Sbjct: 421 KVVHLKGSTGLGFNIVGGEDGE-----GIFVSFILAGGPADLSGELQRGDQILSV--NG 472

Query: 214 SEKNLENTHELAVATLKSIDKVTLI 240  
 + L +HE A A LK VT+I  
 Sbjct: 473 ID--LRGASHEQAAAALKGAGQVTII 497  
 Score = 41.2 bits (95), Expect = 0.10  
 Identities = 24/81 (29%), Positives = 36/81 (43%), Gaps = 6/81 (7%)

Query: 41 IQLERGNISGLGFSIAGGTDNPHIGTDTSIYITKLISGGAAAADGRLXXXXXXXXXXXXX 100  
 + L +G++GLGF+I GG D I+++ +++GG A G L  
 Sbjct: 422 VVLHKGSTGLGFNIVGGEDG-----EGIFVSFILAGGPADLSGELQRGDQILSVNGIDL 475

Query: 101 XXXPHASAVDALKKAGNVVKL 121  
 H A ALK AG V +  
 Sbjct: 476 RGASHEQAAAALKGAGQVTII 496

CLUSTAL W (1.82) sequence alignment

[illegible]

## FIGURE 7

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Hu-Dlg1      ---MPVRKQDTQRALHLLLEEYRSKLSQTEDRQLRSSIERVINIFQSNLFQ-ALIDIQEFY 56
Hu-Dlg4      ---MSQRPRAPRSALWLLAPPLLRWAPP-----LLTVLHSDLFQ-ALLDILDY 45
Hu-Dlg2      ---MFFACYCALRTNVKKYRYQDEDA PHDHS-----LPRLTHEVRGP-ELVHVSEK- 47
Hu-Dlg3      MHKHQHCCCKCECYEVTRLAALRRLEPPGYG-----DWQVPDPYGPGGGNGASAGYGGYS 55
Dm-Dlg1      ---MTTRKK-----KRDGG-----11
Hu-Dlg5      -----

Hu-Dlg1      EVTLLDNPKCIDRSKPSEPIQPVTWEISSLPSTVTSETLPSSLSPSVEKYRYQDEDT 116
Hu-Dlg4      EASLSES-----QKYRYQDEDT 63
Hu-Dlg2      NLSQIEN-----VHGYVLQSHISP 66
Hu-Dlg3      SQTLP SQAG-----ATPTPRTKAKLIP 77
Dm-Dlg1      -----
Hu-Dlg5      -----

Hu-Dlg1      PQEHISPQITNEVIGPELVHVSEKNLSEIENVHGFVSHSHISPIKPT EAVLPSPTVPVI 176
Hu-Dlg4      PLEHSP-----AHLPN-----74
Hu-Dlg2      LK-----68
Hu-Dlg3      TGRDVG-----PVPLKPVPGK-----93
Dm-Dlg1      -----
Hu-Dlg5      -----

Hu-Dlg1      PVLVPVAENTVILPTIPQANPPPVLVNTDSLETP---TYVNGTDADYEYEEITLERNNG 233
Hu-Dlg4      -----QANSEPPVIVNTDTLEAPGYELQVNGTEGEMEYEEITLERNNG 117
Hu-Dlg2      -----ASPAPIIVNTDTLDTIP---YVNGTEIEYEFEEITLERNNG 107
Hu-Dlg3      -----STPKLNGSGPSWWPECTCTNRDWYEQVNGSDGMFKYEEIVLERNNG 140
Dm-Dlg1      -----GSGGGFIKKVSSLFNLD---SVNGDD-SWLYEDIQLERNNG 49
Hu-Dlg5      -----MRATHGSNSLPSSARLGSSSN 21
                ...*

Hu-Dlg1      LGFSIAGGTDNPHIGDDSSIFITKII TGGAAQDGRLRVND CILQVNEVDVRDVTHSKAV 293
Hu-Dlg4      LGFSIAGGTDNPHIGDDPSIFITKII PGGAAQDGRLRVND SILFVNEVDVREVTHSAV 177
Hu-Dlg2      LGFSIAGGTDNPHIGDDPGIFITKII PGGAAEDGRLRVND CILRVNEVDVSEVSHSKAV 167
Hu-Dlg3      LGFSIAGGIDNPHVPDDPGIFITKII PGGAAAMDGR LGVND CVLRVNEVEVSEVHSAV 200
Dm-Dlg1      LGFSIAGGTDNPHIGTDTSIYITKLISGGAAADGR LSIINDIIVSVNDVSVDVPHASAV 109
Hu-Dlg5      LQFKAER-IKIPSTPRYPRSVVGSER--GSVSHSECTPPQSLNIDTLSSCSQSQTAS 78
                * * . * . : . * : . . : : : . . : : *

Hu-Dlg1      EALKEAGSIVRLYVKRRK-----PVS-----EKIMEIKLIKGP KGLGFSI 333
Hu-Dlg4      EALKEAGSIVRLYVMRRK-----PPA-----EKVMEIKLIKGP KGLGFSI 217
Hu-Dlg2      EALKEAGSIARLYVRRR-----PIL-----ETVVEIKLFKGP KGLGFSI 207
Hu-Dlg3      EALKEAGPVVRLVVRRRQ-----PPP-----ETIMEVNLLKGP KGLGFSI 240
Dm-Dlg1      DALKKAGNVVVLHVKKRRK-GTATTPAAGSAAGDARDSAASGPKVIEDLVKGGKGLGFSI 168
Hu-Dlg5      TLPRIAVNPASLGERRKDR---PYV-----EPRHVVKVQKGS EPLGISI 119
                : * . * * : . . : : * : * : *

Hu-Dlg1      AGGVGNQHIPGDNSIYVTKIIEGGAHKD GKLQIGDKLLAVNN---VCLEEVTHEEAVT 389
Hu-Dlg4      AGGVGNQHIPGDNSIYVTKIIEGGAHKD GRLQIGDKILAVNS---VGLEDVMHEDAVA 273
Hu-Dlg2      AGGVGNQHIPGDNSIYVTKIIEGGAHQD GRLQVGDRLLMVNN---YSLEEVTHEEAVA 263
Hu-Dlg3      AGGIGNQHIPGDNSIYITKIIEGGAHQD GRLQIGDRLLAVNN---TNLQDVRHEEAVA 296
Dm-Dlg1      AGGIGNQHIPGDNGIYVTKLTDGGRAQVDGRLSIGDKLIAVRTNGSEKNLENVTHELAVA 228
Hu-Dlg5      VSGE-----KGGIYVSKVTVGSI AHQAG-LEYGDQLLEFNG---INLRSATEQQARL 167
                ..* . . * : : * . * : * * : : . . * . . : *

Hu-Dlg1      ALKNTSDFVYLKVAKPTSMYMDGYA-----415
Hu-Dlg4      ALKN TYDVYLKVAKPSNAYLSDSYA-----299
Hu-Dlg2      ILKNTSEVYLVKGNPTTIYMTDPYG-----289
Hu-Dlg3      SLKNTSDMVYLKVAKPGSLHLNDMYA-----322
Dm-Dlg1      TLKSITDKVTLLIIGKTOHLTTSASGGGGGLSSGQQLSQSQSLATSQSQSQVHQQOAHAT 288
Hu-Dlg5      IIGQQCDTITILAQYNPHVHQLSSHS-----193
                : . : : :

Hu-Dlg1      -----
Hu-Dlg4      -----
Hu-Dlg2      -----
Hu-Dlg3      -----
Dm-Dlg1      -----
Hu-Dlg5      PMVNSQSTGALNSMGQT VVDSPSIPQAAAAVAAAAASASASVIASNTISNTT VTTVTA 348

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[illegible]

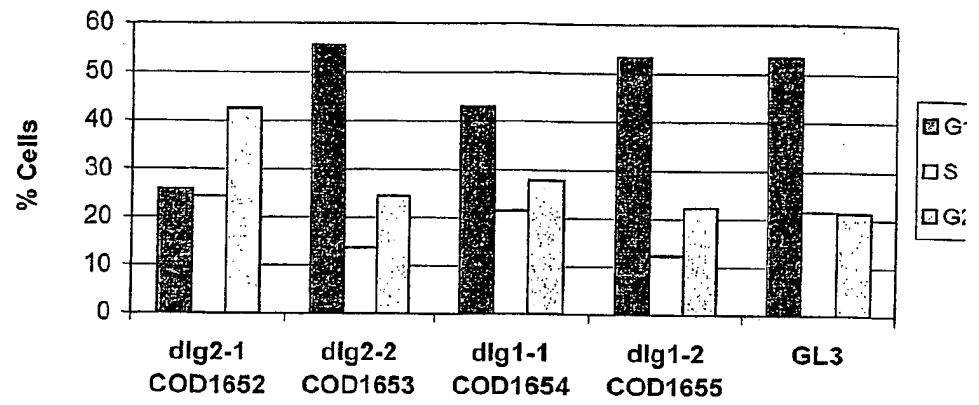


\* .. : \*:: :\*::: :\*: : ..: \*:: \*: ::

Hu-Dlg1 KGKHCILDVSGNAIKRLQIAQLYPISIFIKPKSMENIMEMNK-----RLTEEQARKTFE 877  
 Hu-Dlg4 QGKHCILDVGSANAVRRLQAAHLHPAIFIRPRSLLENVLEINK-----RITEEQARKAFD 718  
 Hu-Dlg2 RGKHCILDVSGNAIKRLQVAQLYPFAIFIKPRSLESLEMEMNK-----RLTEEQAKKTYD 821  
 Hu-Dlg3 RGKHCILDVSGNAIKRLQQAQLYPFAIFIKPKSIEALMEMNR-----RQTYEQANKIYD 768  
 Dm-Dlg1 KGKHCILDVSGNAIKRLQVAQLYPVAVFIKPKSVDSVMEMNR-----RMTEEQAKKTYE 911  
 Hu-Dlg5 KNRHCLLDIAPHAIERLHHMHIYPVIFIFIHYKSAKHIKEQRDPYLRDKVTQRHSKEQFE 626  
 :.:\*::\*::: :\*:::: :\*:::: \* . : \* . : \* :.: : :

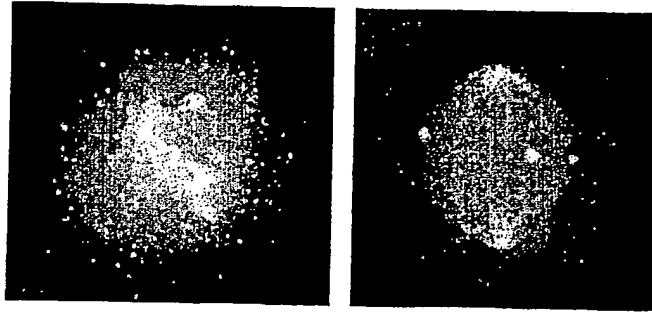
Hu-Dlg1 RAMKLEQEFTEHFTAIVQGDLEDIYNQVKQIIEEQSGSYIWVPAKEKL 926  
 Hu-Dlg4 RATKLEQEFTECFSAIVEGDSFEEIYHKVKRVIEDLSGPYIWVPARERL 767  
 Hu-Dlg2 RAIKLEQEFGEYFTAIVQGDLEDIYNQCKLVIEEQSGPFIWIPSKEKL 870  
 Hu-Dlg3 KAMKLEQEFGEYFTAIVQGDSLEEIYNKIKQIIEEQSGHYIWVPSPEKL 817  
 Dm-Dlg1 RAIKMEQEFGEYFTGVVQGDTEIEIYSKVKSMIWSQSGPTIWVPSKESL 960  
 Hu-Dlg5 AAQKLEQEYSRYFTGVIQGGALSSICTQILAMVNQEONKVLWIPACPL- 674  
 \* \*:\*\*\*: . \*:.....\* : :. . . :\*:::

FIGURE 8

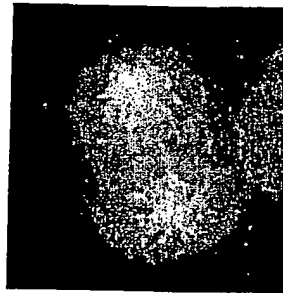


**FIGURE 9**

**A**



**B**



**FIGURE 10**

**A**



**B**

